ALIGNMENT 1: SEQ ID NO:7

Original_Seq? Substitute_Seq? Amended_Seq? Original_Pig4	1 30 31 60 61 90 91 123 GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC GAATTCACGATGGCCAACAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTATAC GAATTCACGATGGCCAACAAAATACAATTCC GAAATCCTGAACAATATCATCCTGAACCTG CGTTACAAAGACAACAATCTGATCGATCTG TCTGGTTACGGTGCTAAAGTTGAAGTTATAC
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Pig4	121 150 151 180 181 210 211 240 GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAG ATCCGTGTTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAG ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAGA ATCCGTGTTACTCAGAATCAGAACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTGACCTCTTCCGCTAACTCTAGA ATCCGTGTTACTCAGAATCAGAACACATCATC TTCAACTCCGTATTCCTGGACTTCTCTGTT GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTCACTCTACGTCAACTCTAGA ATCCGTGTTACTCAGAATCAGAACACACTACT TTCAACTCCGTATTCCTGGACTTCTCTGTT GACGGTGTTGAACTGAATGACAAGAACCAG TTCAAACTCACCTTCTCGCTAACTCTAGA ATCCGTGTTACTCAGAATCAGAACACACTCTTCCCGTATTCCTGGACTTCTCTGTT CAACTCGTATTCCTGGACTTCTCTGTT CAACTCGTATTCTTGTT CAACTCGTATTCTTGTT CAACTCGTATTCTTCTTCTTCTTT CAACTCGTATTCTTCTTTCTTT CAACTCGTATTCTTCTTTCTTTT CAACTCGTATTCTTTCTTTT CAACTCGTATTCTTTCTTTTTT CAACTCGTATTCTTTTTTTTTT
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Pig4	241 270 271 300 301 330 331 360 TCCTTCTGGATHCGTATCCCGAAATCAAG AACGACGGTATCCAGAATTACATCACATA GAATACACCATCATCAACTGCATGAAGAAT AACCTCGGTTGGAAGATCTCCATCCACGGGT TCCTTCTGGATHCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACCTCTGGTTGGAAGATCTCCATCCACCGCGGT TCCTTCTGGATHCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACCTCTGGTTGGAAGATCTCCATCCACGGGT TCCTTCTGGATHCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCACGGGT TCCTTCTGGATHCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCACGGGT TCCTTCTGGATHCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCACGGGT TCCTTCTGGATHCGTATCCCGAAATACAAG AACGACGGTATCCAGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCACGGGT TCCTTCTGGATHCATCACTGAATTACATCACATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCACGGGT TCCTTCTGGATHCATCACTGAATTACATCACATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCACCACATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCACGGGT TCCTTCTGGATHCATCACTGAATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGAATCTCCATCCACGGGT TCCTTCTGGATGATTACATCCACAAT GAATACACCATCATCAACTGCATGAAGAAT AACTCTGGTTGGAAGATCTCCATCCACGGGT TCCTTCTGGATGAATCACACATCAACTGCACATCAACTGCAATGAAGAAT AACTCTGGTTGGAAGAATCTCCATCCACGGGT TCCTTCTGGATGAATCACACATCAACTGCAATGAACACATCAACTGCAATGAAGAAT AACTCTGGTTGGAAGAATCTCCATCCACGGGT TCCTTCTGGATGAATCACACATCAATCAACTGCAATGAAGAAT AACTCTGGTTGGAAGAATCTCCATCCACGATGAATCACACATCAACTGCAATGAATG
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	361 390 391 420 421 450 451 480 AACGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTCGTTACCATCACC AACGGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC AACGGTATCATCTGGACTCTGATCGATATC AACGGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC AACGGTATCATCTGGACTCTGATTCT AACGGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC AACGGTATCATCTGGACTCTGATTCT AACGGTAAGACCAAATCTGTATTCTTCGAA TACAACATCCGTGAAGACATCTCTGAATAC ATCAATCGCTGGTTCTTCGTTACCATCACC
Original_Seg7 Substitute_Seg7 Amended_Seg7 Original_Pig4	481 510 511 540 541 570 571 600 AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGGCTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCGCTAACGGT GAAATCATCTTCAAACTGGACGTGACATC AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCCGTAACGGT GAAATCATCTTCAAACTGGACGTGACATC AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCCGTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC AATAACCTGAACAATGCTAAAATCTACATC AACGGTAAACTGGAATCTAATACCGACATC AAAGACATCCGTGAAGTTATCCGTAACGGT GAAATCATCTTCAAACTGGACGGTGACATC
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	601 630 631 630 631 720 GATGGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGAACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGGACTGTCTCAG GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGGACTGTCTCAG TCCAATATCGAAGAACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAATAC TTCTCCATCTTCAACACCGGACTGTCTCAG TCCAATATCGAAGGACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAGACTGTCTAGACACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAGACTGTCTAGACACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGGATGAAGACTGTCTAGACACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGG GATCGTACCCAGTTCATCTGAACACCGAACTGTCTAGACACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAACACTGTACAGACTGTTCTAGACACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGGAAGACTGTTCTAGACACGGAACTGTCTAGACACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAAGACTTCTGGAAGACTGTCTAGACACGGTACAAGATCCAG TCTTACTCCGAATACCTGAAACACTGAACACTGAACACTGAAACACTGAACACGGTACAAGATCCAGATCAGATCAGACGGTACAAGATCCAGATCAGATCAGATCAGATCAGAACGGTACAAGATCAGATCAGATCAGATCAGATACAAGACGGTACAAGATCAGATCAGATCAGAACGGTACAAGATCAGAACGGTACAAGATCAGATCAGAACGGTACAAGATCAGATCAGATCAGAACGGTACAAGATCAGAACGGTACAAGAACGGTACAAGATCAGAACAGATCAGAACGGTACAAGATCAGAACAGAAGAACGGTACAAGAACGGTACAAGAACGGTACAAGAACGGTACAAGAACGGTACAAGAACGGTACAAGAACACGGAACGGTACAAGAACGGTACAAGAACGGTACAAGAACGGTACAAGAACGGTACAAGAACACGGAACG
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	721 750 751 780 781 810 811 810 811 840 GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAAGAACTCT TACATCAAACTGAAGAAAGACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAACAACTCT TACATCAAACTGAAGAAAACTCTCCGGTT GGTGAAATCCTGACTCGTTCCAAATACAAC GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAACAACTCT TACATCAAACTGAAGAAACACTCTCCGGTT GGTGAAATCCTGACTCGTTTCCAAATACAAC GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAACAACTCT TACATCAAACTGAAGAACACTCTCCGGTT GGTGAAATCCTGACTCGTTTCCAAATACAAC GGTAATCCGCTGATGTACAACAAAGAATAC TATATGTTCAATGCTGGTAACAACAACTCT TACATCAAACTGAAGAACACTCTCCGGTT GGTGAAATCCTGACTCGTTTCCAAATACAAC
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Pig4	841 870 871 900 901 930 931 950 CAGAACTCTAAATACATCACCGCGC CTGTACATCGGTGAAAAGTTCATCATCCCC CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC CAGAACTCTAAATACATCAACTACCGCGC CTGTACATCGGTGAAAAGTTCATCATCCCC CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAGAAGACTACATCTAC CAGAACTCTAAATACATCAACTACCGCGC CTGTACATCGTGAAAAGTTCATCATCCCT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTACGTAAAAGAAGACTACATCTAC CAGAACTCTAAATACATCAACTACCGCGC CTGTACATCGGTGAAAAGTTCATCATCCCT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTAACGAAGACGATCAATCTAC CAGAACTCTAAATACATCAACTACCGCGC CTGTACATCGGTGAAAAGTTCATCATCCCT CGCAAATCTAACTCTCAGTCCATCAATGAT GACATCGTAACGAAGAAGACTACATCTAC CAGAACTCTAAATACATCAACTACCGCGC CTGTACATCGGTGAAAAGTTCATCATCCCT CGCAAATCTAACCTCCAGTCCATCAATGAT GACATCGTAACGAAGAAGACTACATCTAC
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	961 990 991 1020 1021 1050 1051 1080 CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACACTC CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA GAAGAAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACACATC CTGGACTTCTTCAACCTGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA CAAGAAGAAAAAGCTTTTCCTGGCTCCGATC TCTGATTCCGACGAACTCTACAACACACATC CTGGACTTCTTCAACCTGGAATCAGGAATGG CGTGTATACACCTACAAGTACTTCAAGAAA CAAGAAGAAAAAGCTTTTCCTGGCTCCCAAT CTGGATTCCGACGGAACTCTACAACACCATC CTGGACTTCTTCAACCTGGAACGAACTCTACAACACCATC CTGGACTTCTTCAACCTGGAACGAACTCTACAACACCATC CTGGACTTCTTCAACCTGGACCTACAAGTACTTCAAGAAA CAAGAAGAAAAAGCTTTTCCTGGCTCCCAAT CTGGATTCCGACGGAACTCTACAACACCATC CTGGACTTCTTCAACCTGGACGAACTCTACAACACCATC CTGGACTTCTTCAACCTGCAACTACTACAACTACTTCAAGAAA CAAGAAGAAAAAGCTTTTCCTGGCTCCCAAT CTGGATTCCGACGGAACTCTTACAACACCATC CTGGACTTCTTCAACCTGCACGAACTCTTACAACACCATC CTGGACTTCTTCAACCTGCACGAACTCTTACAACACCATC CTGGACTTCTTCAACCTGCACGAACTCTTACAACACCATC CTGGACTTCTTCAACCTGCACGAACTCTTACAACACCATC CTGGACTTCTTCAACCTACAAGTACTTCAAGAAA CTGGACTTCTTCCGACGAACTCTTACAACCACCATC CTGGACTTCTTCAACCTACAAGTACTTCAAGAAA CTGGACTTCTTCCGACGAACTCTTACAACCACCATC CTGGACTTCTTCAACCTACAAGTACTTCAAGAAACACAATACTTCAACACACATC CTGGACTTCTTCAACCTACAAGTACTTCAACACCATC CTGGACTTCTTCAACCTACAAGTACTTCAAGAAAAAACCTTTTCCTGCTCCCAATC CTGGACTTCTTCAACCTACAAGTACTTCAAGAAAAAAACCTTTTCCTGCTCCCAATC CTGGACTTCTTCAACACCTACAAGTACTTCAAGAAAAAAACCTTTTCCTGCTCCCAATC CTGGACTTCTTCAACCTACAAGTACTTCAAGAAAAAACCTTTCAACACCAATC CTGGACTTCTTCAACACAACTACAACTACTACAACTACTTCAACACAACA
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	1081 1110 1111 1140 1141 1170 1170 1200 CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTGTTCAAGAAAGAT GAAGAATCTACTGACGAAATCGGTCTGATC CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTTGTTCAAGAAAGAT CAGATCAAAGAATACGACGAACAGCCGACC TACTCTTGCCAGCTGCTTGTTCAAGAAAGAT CAGATCAAAGAATCGGTCTGATC CAGATCAAAGAATCGGTCTGATCACGAAATCGGTCTGATC CAGATCAAAGAATCTGCTTATCAAGAAAAGATCTGGTTATCAAGAAATCGGTCTGATC CAGATCAAAGAATCGGTCTGATCAACAATCTGGTTATCAAGAAAAGATCTGGTTCTAACGAAATCGGTCTGATC CAGATCAAAGAATCGGTCTGATCAACAATCTGGTATCCACCGTTTCTACGAAATCTGGTATCCACCGTTTCTACGAAATCTGGTATCCACCGTTTCTACGAAATCTGGTATCCACCGTTTCTACGAAATCTGGTATCCACCGTTTCTACGAAATCTGGTATCCACCGTTTCTACGAAATCTGGTATCCACCGTTTCTACGAAATCTGGTATCCACCGTTTCTACGAAACTCTGGTATCCACCGTTTCTACGAAACATCTGGTATCCACCGTTTCTACGAAACTCTGGTATCCACCGTTTCTACGAAACATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTACCACCGTTTCTACGAATCTGGTATCCACCGTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTTCTACGAATCTGGTATCCACCGTTCTACGAATCTGGTATCACCACCGTTCTACCACCGTTCTACCACCGTTCTACACACAC
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	1201 1230 1231 1260 1261 1290 1291 1320 GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAGACGAAGGT GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGGAAGTTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAGACGAAGGT GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAGAGTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAGACGAAGGT GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAAGAGTAAA CGCAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAGACGAAGGT GTATTCGAAGAATACAAAGACTACTTCTGC ATCTCCAAATGGTACCTGAAAGACTAAACCGTACAACCTGAAACTGGGTTGC AATTGGCAGTTCATCCCGAAGACGAAGGT AATTGGCAGTTCATCCCGAAAGACGAAGGT AATTGGCAGTTCATCCCGAAAGACGAAGGAAGT AATTGGCAGTTCATCCCGAAAGACGAAGGAGT AATTGGCAGTTCATCCCGAAAGACGAAGGAAGT AATTGGCAGTTCATCCCGAAAGACGAAGGAGT AATTGGCAGTTCATCCCGAAAGACGAAGGAAGT AATTGGCAGTTCATCCCGAAAGACGAAGGAAGTAAAACGGAAACCGTACAACCTGAAACTGGGTTCC AATTGGCAGTTCATCCCGAAAGACGAAGGAAGTAAACCGTACAACCTGAAACTGGGTTCC AATTGGCAGTTCATCCCGAAAGACGAAGGAAGTAAAAACGGAAACCGTACAACCTGAAACTGGGTTCC AATTGGCAGTTCATCCCGAAAGACGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA
Original_Seq7 Substitute_Seq7 Amended_Seq7 Original_Fig4	1321 TGGACCGAATAGTAAGAATTC TGGACCGAATAGTAAGAATTC TGGACCGAATAGTAAGAATTC TGGACCGAATAGTAAGAATTC

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ALIGNMENT 2: SEQ ID NO:37

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Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	CTCGAGCCATGGCTCGTCTGCTGTCTACCT CTCGAGCCATGGCTCGTCTGCTGTCTACCT CTCGAGCCATGGCTCGTCTGCTGTCTACCT CTCGAGCCATGGCTCGTCTGCTGTCTACCT	TCACTGAATACATCAAGAACATCATCAATA TCACTGAATACATCAAGAACATCAATCAATA TCACTGAATACATCAAGAACATCAATCAATA	CCTCCATCCTGAACCTGCGCTACGAATCCA CCTCCATCCTGAACCTGCGCTACGAATCCA CCTCCATCCTGAACCTGCGCTACGAATCCA CCTCCATCCTGAACCTGCGCTACGAATCCA	91 120 ATCACCTGATCGACCTGTCTCGCTACGCTT ATCACCTGATCGACCTGTCTCGCTACGCTT ATCACCTGATCGACCTGTCTCGCTACGCTT ATCACCTGATCGACCTGTCTCGCTACGCTT ATCACCTGATCGACCTGTCTCGCTACGCTT
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	CCAAAATCAACATCGGTTCTAAAGTTAACT CCAAAATCAACATCGGTTCTAAAGTTAACT CCAAAATCAACATCGGTTCTAAAGTTAACT CCAAAATCAACATCGGTTCTAAAGTTAACT	TCGATCCGATCGACAAGAATCAGATCCAGC TCGATCCGATC	TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG	TTATCCTGAAGAATGCTATCGTATACAACT TTATCCTGAAGAATGCTATCGTATACAACT TTATCCTGAAGAATGCTATCGTATACAACT
Original_Seq37 Substitute_Seq37 Amended_Seq37 Pig2_'975_App	CTATGTACGAAAACTTCTCCACCTCCTTCT CTATGTACGAAAACTTCTCCACCTCCTTCT CTATGTACGAAAACTTCTCCACCTCCTTCT CTATGTACGAAAACTTCTCCACCTCCTTCT	GGATCCGTATCCCHAAATACTTCAACTCCA	TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA	ACTGCATGGAAAACAATTCTGGTTGGAAAG
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	TATCTCTGAACTACGGTGAAATCATCTGGA TATCTCTGAACTACGGTGAAATCATCTGGA TATCTCTGAACTACGGTGAAATCATCTGGA TATCTCTGAACTACGGTGAAATCATCTGGA	CTCTGCAGGACACTCAGGAAATCAAACAGC CTCTGCAGGACACTCAGGAAATCAAACAGC CTCTGCAGGACACTCAGGAAATCAAACAGC	GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA	ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	TCGTTACCATCACCAACAATCGTCTGAATA TCGTTACCATCACCAACAATCGTCTGAATA TCGTTACCATCACCAACAATCGTCTGAATA TCGTTACCATCACCAACAATCGTCTGAATA	ACTCCAAAATCTACATCAACGGCCGTCTGA	TCGACCAGAAACCGATCTCCAATCTGGGTA TCGACCAGAAACCGATCTCCAATCTGGGTA TCGACCAGAAACCGATCTCCAATCTGGGTA	571 600 ACATCCACGETTCTAATAACATCATGTTCA ACATCCACGETTCTAATAACATCATGTTCA ACATCCACGETTCTAATAACATCATGTTCA ACATCCACGETTCTAATAACATCATGTTCA
Original Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	AACTGGACGGTTGTCGTGACACTCACCGCT AACTGGACGGTTGTCGTGACACTCACCGCT AACTGGACGGTTGTCGTGACACTCACCGCT AACTGGACGGTTGTCGTGACACTCACCGCT	631 660 ACATCTIGGATCANATACTTCAATCTGTTCG ACATCTIGGATCANATACTTCAATCTGTTCG ACATCTIGGATCANATACTTCAATCTGTTCG ACATCTIGGATCANATACTTCAATCTGTTCG	ACAAAGAACTGAACGAAAAAGAAATCAAAG ACAAAGAACTGAACGAAAAAGAAATCAAAG ACAAAGAACTGAACGAAAAAAAAAA	ACCTGTACGACAACCAGTCCAATTCTGGTA ACCTGTACGACAACCAGTCCAATTCTGGTA ACCTGTACGACAACCAGTCCAATTCTGGTA
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	TCCTGAAAGACTTCTGGGGTGACTACCTGC TCCTGAAAGACTTCTGGGGTGACTACCTGC TCCTGAAAGACTTCTGGGGTGACTACCTGC TCCTGAAAGACTTCTGGGGTGACTACCTGC	751 780 AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC	TGTACGATCCGAACAAATACGTTGACGTCA TGTACGATCCGAACAAATACGTTGACGTCA TGTACGATCCGAACAAATACGTTGACGTCA XTACGATCCGAACAAATACGTTGACGTCA	ACAATGTAGGTATCCGCGGTTACATGTACC ACAATGTAGGTATCCGCGGGTTACATGTACC
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	TGAAAGGTCCGCGTGGTTCTGTTATGACTA TGAAAGGTCCGCGTGGTTCTGTTATGACTA TGAAAGGTCCGCCTGGTTCTGTTATGACTA	871 900 CCAACATCTACCTGAACTCTTCCCTGTACC CCAACATCTACCTGAACTCTTCCCTGTACC CCAACATCTACCTGAACTCTTCCCTGTACC CCAACATCTACCTGAACTCTTCCCTGTACC	GTGGTACCAAATTCATCATCAAGAAATACG GTGGTACCAAATTCATCATCAAGAAATACG GTGGTACCAAATTCATCAATCAAGAAATACG GTGGTACCAAATTCATCATCAAGAAATACG	CGTCTGGTAACAAGGACAATATTGGTCGGCA CGTCTGGTAACAAGGACAATATTGGTCGCA
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_'975_App	ACAATGATCGTGTATACATCAATGTTGTAG ACAATGATCGTGTATACATCAATGTTGTAG ACAATGATCGTGTATACATCAATGTTGTAG	991 1020 TTAAGAACAAAGAATACCGTCTGGCTACCA TTAAGAACAAAGAATACCGTCTGGCTACCA TTAAGAACAAAGAATACCGTCTGGCTACCA TTAAGAACAAAGAATACCGTCTGGCTACCA	ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT	TGTCTGCTCTGGAAATCCCGGACGTTGGTA TGTCTGCTCTGGAAATCCCGGACGTTGGTA TGTCTGCTCTGGAAATCCCGGACGTTGGTA TGTCTGCTCTGGAAATCCCGGACGTTGGTA
Original_Seq17 Substitute_Seq17 Amended_Seq17 Pig2_'975_App	ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA	1111 1140 AGAACGACCAGGGTATCACTAACAANTGCA AGAACGACCAGGGTATCACTAACAANTGCA AGAACGACCAGGGTATCACTAACAANTGCA AGAACGACCAGGGTATCACTAACAANTGCA	AAATGAATCTGCAGGACAACAATGGTAACG AAATGAATCTGCAGGACAACAATGGTAACG AAATGAATCTGCAGGACAACAATGGTAACG AAATGAATCTGCAGGACAACAATGATAACGAAATGAATAACGAAATGAATAACGAAATGAATAACGAAATGAAAACAAATGAAAAAAAA	ATATCGGTTTCATCGGTTTCACCAGTTCA ATATCGGTTTCATCGGTTTCACCAGTTCA ATATCGGTTTCATCGGTTTCACCACTTCA ATATCGGTTTCATCGGTTTCACCACTTCA
Original_Seq17 Substitute_Seq17 Amended_Seq17 Fig2_'975_App	ACAATATCGCTAAACTGGTTGCTTCCAACT ACAATATCGCTAAACTGGTTGCTTCCAACT ACAATATCGCTAAACTGGTTGCTTCCAACT	1231 1260 GGTACAATCGTCAGATCGAACGTTCCTCTC GGTACAATCGTCAGATCGAACGTTCCTCTC GGTACAATCGTCAGATCGAACGTTCCTCTC GGTACAATCGTCAGATCGAACGTTCCTCTC	GCACTCTGGGTTGCTCTTGGGAGTTCATCC GCACTCTGGGTTGCTCTTGGGAGTTCATCC GCACTCTGGGTTGCTCTTGGGAGTTCATCC GCACTCTAGGTTGCTCTTGGGAGTTCATCC	CGGTTGATGACGGTTGGGGTGAACGTCCGC CGGTTGATGACGGTTGGGGTGAACGTCCGC CGGTTGATGACGGTTTGGGTGAACGTCCGC
Original_Seq37 Substitute_Seq37 Amended_Seq37 Pig2_'975_App	1321 1338 TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT			

NY02:465989.1

ALIGNMENT 3: SEQ ID NO:39

Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	ATGGCTTTCAACAATACAATTCCGAAATC ATGGCTTCAACAATACAAT	CTGAACAATATCATCCTGAACCTGCGTTAC CTGAACAATATCATCCTGAACCTGCGTTAC CTGAACAATATCATCCTGAACCTGCGTTAC CTGAACAATATCATCCTGAACCTGCGTTAC	AAAGACAACAATCTGATCGATCTGTCTGGT AAAGACAACAATCTGATCGATCTGTCTGGT AAAGACAACAATCTGATCGATCTGTCTGGT	91 120 TACGGTGCTAAAGTTGAAGTATACGACGGT TACGGTGCTAAAGTTGAAGTATACGACGGT TACGGTGCTAAAGTTGAAGTATACGACGGT TACGGTGCTAAAGTTGAAGTATACGACGGT TACGGTGCTAAAGTTGAAGTATACGACGGT
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	GTTGAACTGAATGACAAGAACCAGTTCAAA GTTGAACTGAATGACAAGAACCAGTTCAAA GTTGAACTGAATGACAAGAACCAGTTCAAA GTTGAACTGAATGACAAGAACCAGTTCAAA	CTGACCTCTTCCGCTAACTCTAAGATCCGT CTGACCTCTTCCGCTAACTCTAAGATCCGT CTGACCTCTTCCGCTAACTCTAAGATCCGT CTGACCTCTTCCGCTAACTCTAAGATCCGT		TCCGTATTCCTGGACTTCTCTGTTTCCTTC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	TGGATCCGTATCCCGAAATACAAGAACGAC TGGATCCGTATCCCGAAATACAAGAACGAC TGGATCCGTATCCCGAAATACAAGAACGAC	GGTATCCAGAATTACATCCACAATGAATAC GGTATCCACAATTACATCACCAATGAATAC GGTATCCAGAATTACATCCACAATGAATAC GGTATCCAGAATTACATCACCATGAATAC	301 330 ACCATCATCAACTGCATGAAGAATAACTCT ACCATCATCAACTGCATGAAGAATAACTCT ACCATCATCAACTGCATGAAGAATAACTCT ACCATCATCAACTGCATGAAGAATAACTCT	GGTTGGAAGATCTCCATCCGCGGTAACCGT GGTTGGAAGATCTCCATCCGCGGTAACCGT GGTTGGAAGATCTCCATCCGCGTAACCGT
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	ATCATCTGGACTCTGATCGATATCAACGGT ATCATCTGGACTCTGATCGATATCAACGGT ATCATCTGGACTCTGATCGATATCAACGGT	AAGACCAAATCTGTATTCTTCGAATACAAC AAGACCAAATCTGTATTCTTCGAATACAAC AAGACCAAATCTGTATTCTTCGAATACAAC AAGACCAAATCTGTATTCTTCGAATACAAC	421 450 ATCCGTGAAGACATCTCTGAATACATCAAT ATCCGTGAAGACATCTCTGAATACATCAAT ATCCGTGAAGACATCTCTGAATACATCAAT ATCCGTGAAGACACTCTCTGAATACATCAAT	CGCTGGTTCTTCGTTACCATCACCAATAAC CGCTGGTTCTTCGTTACCATCACCAATAAC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	CTGAACAATGCTAAAATCTACATCAACGGT CTGAACAATGCTAAAATCTACATCAACGGT CTGAACAATGCTAAAATCTACATCAACGGT CTGAACAATGCTAAAATCTACATCAACGGT	AAACTGGAATCTAATACCGACATCAAAGAC AAACTGGAATCTAATACCGACATCAAAGAC AAACTGGAATCTAATACCGACATCAAAGAC	541 570 ATCGGTGAAGTTATCGCTAACGGTGAAATC ATCCGTGAAGTTATCGCTAACGGTGAAATC ATCCGTGAAGTTATCGCTAACGGTGAAATC ATCCGTGAAGTTATCGCTAACGGTGAAATC	ATCTTCAAACTGGACGTGACATCGATCGT
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	ACCCAGTTCATCTGGATGAAATACTTCTCC ACCCAGTTCATCTGGATGAAATACTTCTCC ACCCAGTTCATCTGGATGAAATACTTCTCC	ATCITCAACACCGAACTGTCTCAGTCCAAT ATCITCAACACCGAACTGTCTCAGTCCAAT ATCITCAACACCGAACTGTCTCAGTCCAAT	ATCGAAGAACGGTACAAGATCCAGTCTTAC ATCGAAGAACGGTACAAGATCCAGTCTTAC ATCGAAGAACGGTACAAGATCCAGTCTTAC ATCGAAGAACGGTACAACATCAGTCTTAC	TCCGAATACCTGAAAGACTTCTGGGGTAAT TCCGAATACCTGAAAGACTTCTGGGGTAAT TCCGAATACCTGAAAGACTTCTGGGGTAAT
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	CCOCIONIGINCHACAMOMIACIAIAIG	TTCAATGCTGGTAACAAGAACTCTTACATC TTCAATGCTGGTAACAAGAACTCTTACATC TTCAATGCTGGTAACAAGAACTCTTACATC TTCAATGCTGGTAACAACAACTCTTACATC	AAACTGAAGAAAGACTCTCCGGTTGGTGAA AAACTGAAGAAAGACTCTCCGGTTGGTGAA AAACTGAAGAAAGACTCTCCGGTTGGTGAA	STCCTGACTCGTTCCAAATACAACCAGAAC ATCCTGACTCGTTCCAAATACAACCAGAAC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	841 870 TCTAAATACATCAACTACCGCGACCTGTAC TCTAAATACATCAACTACCGCGACCTGTAC TCTAAATACATCAACTACCGCGACCTGTAC TCTAAATACATCAACTACCGCGACCTGTAC	ATCGGTGAAAAGTTCATCATCCGTCGCAAA ATCGGTGAAAAGTTCATCATCCGTCGCAAA ATCGGTGAAAAGTTCATCATCATCGCAAA ATCGGTGAAAAGTTCATCATCCGTCGCAAA	TCTAACTCTCAGTCCATCAATGA GACATC TCTAACTCTCAGTCCATCAATGA GACATC TCTAACTCTCAGTCCATCAATGA GACATC TCTAACTCTCAGTCCATCAATGA GACATC	GTACGTAAAGAAGACTACATCTACCTGGAC GTACGTAAAGAAGACTACATCTACCTGGAC GTACGTAAAGAAGACTACATCTACCTGGAC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	961 990 TTCTTCAACCTGAATCAGTAATGGCGTGTA TTCTTCAACCTGAATCAGTAATGGCGTGTA TTCTTCAACCTGAATCAGTAATGGCGTGTA TTCTTCAACCTGAATCAGTAATGGCGTGTA TTCTTCAACCTGAATCAGTAATGGCGTGTA	TACACCTACAAGTACTTCAAGAAGAAGAA TACACCTACAAGTACTTCAAGAAGAAGAA TACACCTACAAGTACTTCAAGAAGAAGAAGAA TACACCTACAAGTACTTCAAGAAGAAGAAGAA	GAAAAGCTTTTCCTGGCTCCGATCTCTGAT GAAAAGCTTTTCCTGGCTCCGATCTCTGAT GAAAAGCTTTTCCTGGCTCCGATCTCTGAT	TCCGACGAACTCTACAACACCATCCAGATC TCCGACGAACTCTACAACACCATCCAGATC TCCGACGAACTCTACAACACCATCCAGATC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	1081 1110 AAAGAATACGACGAACAGCCGACCTACTCT AAAGAATACGACGAACAGCCGACCTACTCT AAAGAATACGACGAACAGCCGACCTACTCT AAAGAATACGACGAACAGCCGACCTACTCT AAAGAATACGACGAACAGCCGACCTACTCT	TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TGCCAGCTGCTGTTCAAGAAAGATGAAGAA TGCCAGCTGCTGTTCAAGAAAGATGAAGAA	TCTACTGACGAAATCGGTCTGATCGGTATC TCTACTGACGAAATCGGTCTGATCGGTATC TCTACTGACGAAATCGGTCTGATCGGTATC	CACCGTTTCTACGAATCTGGTATCGTATTC CACCGTTTCTACGAATCTGGTATCGTATTC CACCGTTTCTACGAATCTGGTATCGTATTC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Fig4_'975_App	1201 1230 GAAGAATACAAAGACT CTTCTGCATCTCC GAAGAATACAAAGACT CTTCTGCATCTCC GAAGAATACAAAGACT CTTCTGCATCTCC GAAGAATACAAAGACT CTTCTGCATCTCC GAAGAATACAAAGACT CTTCTGCATCTCC	AAATGGTACCTGAAGGAAGTTAAACGCAAA AAATGGTACCTGAAGGAAGTTAAACGCAAA AAATGGTACCTGAAGGAAGTTAAACGCAAA AAATGTACCTGAAGGAAGTTAAACGCAAA	CCGTACAACCTGAAACTGGGTTGCAATTGG CCGTACAACCTGAAACTGGGTTGCAATTGG CCGTACAACCTGAAACTGGGTTGCAATTGG	CAGTTCATCCCGAAAGACGAAGGTTGGACC CAGTTCATCCCGAAAGACGAAGGTTGGACC CAGTTCATCCCGAAAGACGAAGGTTGGACC
Original_Seq39 Substitute_Seq39 Amended_Seq39 Pig4_'975_App	1321 1350 GAATAGTAACCTCTAGAGTCGAGGCCTGCA GAATAGTAACCTCTAGAGTCGAGGCCTGCA GAATAGTAACCTCTAGAGTCGAGGCCTGCA GAATAGTAACCTCTAGAGTCGAGGCCTGCA GAATAGTAACCTCTAGAGTCGAGGCCTGCA	9 9 9		

ALIGNMENT 4: SEQ ID NO:40

Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186		31 60	61 90	91 120
	mpvtinnfnyndpidnnniimmeppfargt	GRYYKAFKITDRIWIIPERYTFGYKPEDFN	KSSGI FNRDVCEYYDPDYLMTNDKKN I FLQ	TMIKLPNRIKSKPLGEKLLEMIINGIPYLG
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186		•••••••••••••••••••••••••••••••••••••••		
	DRRVPLEEPNTNIASVTVNKLISNPGEVER . 241 270			GASIFNRRGYFSDPALILMHELIHVLHGLY 331 360
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186				
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186			421 450	
**************************************				nedlffi adknspsddlskner i byntosn
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186			541 570 LYSQTFPLDIRDISLTSSFDDALLFSNKVY	SPFSMDYIKTANKVVEAGLFAGWVKQIVND
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186				691 720 EKWSDMYGLIVAQWLSTVNTQPYTIKEGMY
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	721 750 KALNYQAQALEE1IKYRYNIYSEKEKSNIN		***************************************	***************************************
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	841 870	871 900 KDNNLI I DLSGYGAKVEVYDGVELNDKNOFK KDNNLI I DLSGYGAKVEVYDGVELNDKNOFK KDNNLI I DLSGYGAKVEVYDGVELNDKNOFK KDNNLI I DLSGYGAKVEVYDGVELNDKNOFK	901 930 LTSSANSKIRVTQNQNIIFNSVFLDFSVSP LTSSANSKIRVTQNQNIIFNSVFLDFSVSP LTSSANSKIRVTQNQNIIFNSVFLDFSVSF	931 960 WIRIPKYKNDGIQNYIHNBYTIINCMKNNS WIRIPKYKNDGIQNYIHNBYTIINCMKNNS WIRIPKYKNDGIQNYIHNBYTIINCMKNNS
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	961 990 GMKISIRGNRIÜMTLIDINGKTKSVFPEYN GWKISIRGNRIÜMTLIDINGKTKSVFFEYN GMKISIRGNRIÜMTLIDINGKTKSVFFEYN GMKISIRGNRIÜMTLIDINGKTKSVFEYN	IREDISEYINRWPPVTITNNLNNAKIYING IREDISEYINRWPPVTITNNLNNAKIYING IREDISEYINRWPPVTITNNLNNAKIYING IREDISEYINBWPPVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIPKLDGDIDR KLESNTDIKDIREVIANGEIIPKLDGDIDR KLESNTDIKDIREVIANGEIIPKLDGDIDR	TQPIWMKYPSIFNTELSQSNIBERYKIQSY TQPIWMKYPSIFNTELSQSNIBERYKIQSY TQPIWMKYPSIFNTELSQSNIBERYKIQSY
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	1081 1110 SEYLKDPWGNPLMYNKEYYMFNAGNKNSYI SEYLKDPWGNPLMYNKEYYMFNAGNKNSYI SEYLKDPWGNPLMYNKEYYMFNAGNKNSYI SEYLKDPWGNPLMYNKEYYMFNAGNKNSYI	KLKKDSPYGEILTRSKYNONSKYINYRDLY KLKKDSPYGEILTRSKYNONSKYINYRDLY KLKKDSPYGEILTRSKYNONSKYINYRDLY KLKKDSPYGEILTRSKYNONSKYINYRDLY	IGEKFIIRRKSNSQSINDDIVRKEDYIYLD IGEKFIIRRKSNSQSINDDIVRKEDYIYLD IGEKFIIRRKSNSQSINDDIVRKEDYIYLD IGEKFIIRRKSNSQSINDIVRKEDYIYLD	FFNLNOETRYTYKEPKKEEEKLFLAPISD FFNLNOETRYYTYKYPKKEEKLFLAPISD FFNLNOETRYTYKYFKKEEKLFLAPISD
Original_Seq40 Substitute_Seq40 Amended_Seq40 Whelan_M81186	1201 1230 SDEPYNTIQIKEYDEQPTYSCOLLPKKDEE SDEPYNTIQIKEYDEQPTYSCOLLPKKDEE SDEPYNTIQIKEYDEQPTYSCOLLPKKDEE SDEPYNTIQIKEYDEQPTYSCOLLPKKDEE	STDEIGLIGIHRPYESGIVFEEYKDYPCIS STDEIGLIGIHRPYESGIVFEEYKDYPCIS STDEIGLIGIHRPYESGIVFEEYKDYFCIS STDEIGLIGIHPPYESGIVFEFYKDYPCIS	KWYLKEVKRKPYNLKLGCNWOPIPKDEGWT KWYLKEVKRKPYNLKLGCNWOPIPKDEGWT KWYLKEVKRKPYNLKLGCNWOPIPKDEGWT	E E E

ALIGNMENT 5: SEQ ID NO:41

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Original_Seq41 Substitute_Seq41 Amended_Seq41	1 30	31 60	61 90	91 120
Thompson_X52066	MQFVNKQFNYKDPVNGVDIAYIKIPNVGQM	QPVKAFKIHNKIWVIPERDTFTNPEEGDLN	PPPEAKQVPVSYYDSTYLSTDNEKDNYLKG	VTKLFBRIYSTDLGRMLLTSIVRGIPFWGG
Original_Seq41 Substitute_Seq41 Amended_Seq41	121 150	151 180	181 210	211 240
Thompson_X52066			GSTQYIRFSPDFTFGFEESLEVDTNPLLGA	GKFATDPAVTLAHELIHAGHRLYGIA INPN
Original_Seq41 Substitute_Seq41 Amended_Seq41		***************************************	***************************************	
Thompson_X52066			KSIVGTTASLQYNKNVFKEKYLLSEDTSGK	
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066		***************************************		NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
			\$6.7 \$1.2	
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	ITSDTNIEAAEENISLDLIQQYYLTPNPDN ITSDTNIEAAEENISLDLIQQYYLTPNPDN ITSDTNIEAAEENISLDLIQQYYLTPNPDN ITSDTNIEAAEENISLDLIQQYYLTPNPDN ITSDTNIEAAEENISLDLIQQYYLTPNPDN	EPENISIENLSSDIIGQLELMPNIERFPNG EPENISIENLSSDIIGQLELMPNIERFPNG EPENISIENLSSDIIGQLELMPNIERFPNG EPENISIENLSSDIIGOLELMPNIERFPNG	KKYELDKYTMFHYLRAQEFEHGKSRIALTN KKYELDKYTMFHYLRAQEFEHGKSRIALTN KKYELDKYTMFHYLRAQEFEHGKSRIALTN KKYELDKYTMFHYLRAQEFEHGKSRIALTN	SVNEALLNPSRVYTPFSSDYVKKVNKATEA SVNEALLNPSRVYTPFSSDYVKKVNKATEA SVNEALLNPSRVYTFPSSDYVKKVKATEA SVNEALLNPSRVYTPPSSDYVKKVNATEA
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	AMFLGWVEQLVYDFTDETSEVSTTDKIADI AMFLGWVEQLVYDFTDETSEVSTTDKIADI AMFLGWVEQLVYDFTDETSEVSTTDKIADI AMFLGWVEQLVYDFTDETSEVSTTDKIADI	TIIIPYIGPALNIG MLYKDDFVGALIFSG TIIIPYIGPALNIG MLYKDDFVGALIFSG TIIIPYIGPALNIG MLYKDDFVGALIFSG TIIIPYIGPALNIG MLYKDDFVGALIFSG	690 AVILLEPI PEIAI PVLGTFALVSYI ANKVL	TVQTIDNALSKRNEKWDEVYKYIVTNWLAK
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	VNTQIDLIRKMKEALENQAEATKAIINYQ VNTQIDLIRKMKEALENQAEATKAIINYQ VNTQIDLIRKMKEALENQAEATKAIINYQ	YNQYTEEEKNN INFN I DDLSSKLNES INKA YNQYTEEEKNN INFN I DDLSSKLNES INKA YNQYTEEEKNN INFN I DDLSSKLNES INKA YNOYTEEEKNN INFN I DDLSSKLNES INKA	781 MININKPLNQCSVSYLMNSMIPYGVKRLED MININKPLNQCSVSYLMNSMIPYGVKRLED MININKPLNQCSVSYLMNSMIPYGVKRLED MININKPLNQCSVSYLMNSMIPYGVKRLED	FDASLKDALLKYIRDNYGTLIGOVDRLKDK FDASLKDALLKYIRDNYGTLIGOVDRLKDK FDASLKDALLKYIRDNYGTLIGOVDRLKDK
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI VNNTLSTDIPFQLSKYVDNQRLLSTFTEYI	KNIINTSILNLRYESNHLIDLSRYASKINI KNIINTSILNLRYESNHLIDLSRYASKINI KNIINTSILNLRYESNHLIDLSRYASKINI KNIINTSILNLRYESNHLIDLSRYASKINI	930 GSKVNPDPIDKNQIQLPNLESSKIEVILKN GSKVNPDPIDKNQIQLPNLESSKIEVILKN GSKVNPDPIDKNQIQLPNLESSKIEVILKN GSKVNPDPIDKNQIQLPNLESSKIEVILKN	AIVYNSMYENPSTSPWIRIPKYPNSISLMN AIVYNSMYENPSTSPWIRIPKYPNSISLMN AIVYNSMYENPSTSPWIRIPKYPNSISLMN
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	EYTI INCMENNSGWKVSLNYGEI IWTLODT EYTI INCMENNSGWKVSLNYGEI IWTLODT	QEIKQRVVFKYSQMINISDYINRWIFVTIT QEIKQRVVFKYSQMINISDYINRWIFVTIT QEIKQRVVFKYSQMINISDYINRWIFVTIT OEIKQRVVFKYSOMINISDYINRWIFVTIT	1021 INDIANSKIY II INGRLIDOKPI SNLGNIHA INNILINISKIY II INGRLIDOKPI SNLGNIHA INNILINISKIY II INGRLIDOKPI SNLGNIHA INNILINISKIY II INGRLIDOKPI SNLGNIHA INGRLIDOKPI SNLGNIHA	SNN IMPKLDGCRDTHRY I WI KYPNLFDKEL SNN IMPKLDGCRDTHRY I WI KYPNLPDKEL SNN IMPKLDGCRDTHRY I WI KYPNLPDKEL
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52066	NEKEIKDLYDNQSNSGILKDFWGDYLQYDK NEKEIKDLYDNQSNSGILKDFWGDYLQYDK	PYYMTILYDPNKYVDVNNVGIRGYMYLKGP PYYMTILYDPNKYVDVNNVGIRGYMYLKGP PYYMTILYDPNKYVDVNNVGIRGYMYLKGP PYYMTILYDPNKYVDVNNVGIRGYMYLKGP	1140 RGSVMTTNIYLNSSLYRGTKFIIKKÄASGN RGSVMTTNIYLNSSLYRGTKFIIKKÄASGN RGSVMTTNIYLNSSLYRGTKFIIKKÄASGN RGSVMTTNIYLNSSLYRGTKFIIKKÄASGN	KDN I VRNNDRVY I NVVVKNKEYRLATNASQ KDN I VRNNDRVY I NVVVKNKEYRLATNASQ KDN I VRNNDRVY I NVVVKNKEYRLATNASQ
Original_Seq41 Substitute_Seq41 Amended_Seq41 Thompson_X52065	1201 1230 AGVEKILSALEIPDVGNLSQVVVMKSKNDQ AGVEKILSALEIPDVGNLSQVVVMKSKNDQ AGVEKILSALEIPDVGNLSQVVVMKSKNDQ AGVEKILSALEIPDVGNLSQVVVMKSKNDQ	GITNKCKMNLQDNNGNDIGFIGFHQFNNIA GITNKCKMNLQDNNGNDIGFIGFHQFNNIA GITNKCKMNLQDNNGNDIGFIGFHQFNNIA GITNKCKMNLQDNNGNDIGFIGFNOFNNIA	KLVASNWYN ETERSSRTLGCSWEF I PVDD KLVASNWYN GOERSSRTLGCSWEF I PVDD KLVASNWYN GOERSSRTLGCSWEF I PVDD KLVASNWYN FOR FRSSPTLGCSWEF I DVDD KLVASNWYN FOR FRSSPTLGCSWEF I DVDD	GWGERPL GWGERPL GWGERPL

ALIGNMENT 6: SEQ ID NO:42

				
	1 30	31 60	61 90	91 120
Original Seq42				
Substitute_Seq42		***************************************	•••••	
Amended Seq42				
Whelan_M81186	mpvtinnfnyndpidnnniimmeppfargt	GRYYKAFKITDRIWIIPERYTFGYKPEDFN	KSSGI PNRDVÇEYYDPDYLNINDKKNI PLQ	TMIKLFNRIKSKPLGEKLLEMIINGIPYLG
	121	153	101	211
Original Seq42	121 150	151 180	181 210	211 240
Substitute_Seq42		***************************************		
Amended_Seq42				
Whelan M81186	DRRVPLEEFNTN I ASVTVNKL I SNPGEVER	KKGIFANLIIFGPGPVLNENETIDIGIONH	FASREGFGG I MOMKFCPEYVSVFNNVOENK	GASIFNRRGYFSDPALILMHELIHVLHGLY
-		-		
Outstanl Comta	241 270	271 300	301 330	331 360
Original_Seq42 Substitute_Seq42		***************************************		•••••
Amended Seq42	***************************************		***************************************	
Whelan_M81186			DRLNKVLVCISDPNININIYKNKPKDKYKF	
-				
		•••		
Original_Seq42		391 420	1001010ID	451 480
Substitute_Seq42			APGICIDVD	NEDLEF LADKING SODIL STORES LEGISLATION
Amended Seq42		***************************************	APGICIDVD	MEDIT PET YEAR SECOND CAMES LEAVEN ON
Whelan M81186	IAENYKIKTRASYFSDSLPPVKIKNLLDNR	IYTIREGENI SDKDMEKEYRGONKA INKOA	YEEISKEHLAVYKIQMCKSVKAPGICIDVD	NEDLEFTADINGFEDDLEAMERTETATON
		The state of the s	* * * * * * * * * * * * * * * * * * *	NEDDI TADAMENTANI
			top as see a district	
	481 510			571 600
Original_Seq42	YIENDFPINELILDTDLISKIELPSENTES	LTDPNVDVPVYEKQPAIKK1PTDENT1FQY	LYSQTFPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLFAGWVKQIVND
Substitute_Seq42	YIENDFPINELILDTDLISKIELPSENTES	LTDPNVDVPVYEKQPA I KK I PTDENT I FQY	LYSQTPPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLFAGWVKQIVND
Amended_Seq42	YIENDFPINELILDTDLISKIELPSENTES	LTDFNVDVPVYEKQPAIKKIFTDENTIFQY	LYSQTFPLDIRDISLTSSFDDALLFSNKVY	SFPSMDYIKTANKVVEAGLPAGWVKQIVND
Whelan_M81186	TIENDPPINELILDIDLISKIELPSENTES	LIDPNVDVPVYEKQPAIKKIPIDENTIPQY	LYSOTFPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLPAGWVKQIVND
	tan municipalities	transference on the account of the party of the		CO. Marie Company of the company of
	601 630		661 690	691 720
Original_Seq42	FVIEANKSNTMDK1ADISLIVPYIGLALNV	GNETAKGNPENAPE I AGAS I LLEF I PELLI	PVVGAFLLESYIONKNKIIKTIONALTKRN	EKWSDMYGLIVAQWLSTVNTQFYTIKEGMY
Substitute_Seq42	FVIEANKSNIMDKIADISLIVPYIGLALNV	GNETAKGNPENAPEIAGAS ILLEF I PELLI	PVVGAFLLESYIDNKNKIIKTIDNALTKRN	EXWSDMYGLIVAQWLSTVMTQFYTIKEGMY
Amended_Seq42	PVIKANKSNIMDKIADISLIVPYIGLALNV	GNETAKGNFENAPEIAGASILLEFIPELLI	PVVGAFLLESYIDNKNKIIKTIDNALTKRN	EKWSDMYGLIVAOWLSTVNTOFYTIKEGMY
Whelan_M81186	PVIEANKSNIMDKIADISLIVPYIGLALNV	GNETAKGNFENAFEIAGASILLEFIPELLI	PVVGAFLLESYIDNKNK11KT1DNALTKRN	EKWSDMYGLIVAQWLSTVNTQPYTIKEGMY
	Colored Colored Anna Colored C			
	721 750	751 780	781 810	811 840
Original_Seq42	KALNYQAQALEEIIKYRYNIYSEKEKSNIN		SYLMKKMI PLAVEKLLDPDNTLKKNLLNYI	DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
Substitute_Seq42	Kalnyqaqaleeiikyryniysekeksnin	IDFNDINSKLNEGINQAIDNINNFINGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI	DENKLYLIGSAEYEKSKVNKYLKTIMPFDL
Amended_Seq42	KALNYQAQALEEIIKYRYNIYSEKEKSNIN	IDFNDINSKLNEGINOAIDNINNFINGCSV	SYLMKKMI PLAVEKLI DEDNTI KKNI LINYI	DENKLYLICSARVEKSKUNKYLKTIMDEDI.
Whelan_M81186	KALNYOAOALEEIIKYRYNIYSEKEKSNIN	IDENDINSKLNEGINGAIDNINNFINGCSV	SVIMERMIDIAUPELL DEDNITE REMIT MY I	DENVI VI TOCKOVOVOVINIVVI PTIMODOI
	ran James Marsalan Jan, Charles et Visignasse	Parameter and the Committee of the Commi		The second secon
	841 870	871 900	901 930	931 960
Original_Seq42	SIYTNDTILIEMFNKYNSEILNNIILNLRY	KDNNLIDLSGYGAKVEVYDGVELNDKNOPK	LTSSANSK IRRTONONI I PNSVPLDRSVSR	MIDIDEVENDE LONGIUMENTI INCMENTIC
Substitute_Seq42	SIYTNDTILIEMFNKYNSEILNNIILNLRY	KDNNL1DLSGYGAKVEVYDGVELNDKNOFK	LTSSANSKIRMTONONIIFNSVFLDFSVSF	WIRIPKYKNDGIONYIHNRYTTINCHKNNS
Amended_Seq42	SIYTNDTILIEMFNKYNSEILNNIILNLRY SIYTNDTILIEMFNKYNSEILNNIILNLRY SIYTNDTILIEMFNKYNSEILNNIILNLRY	KDNNLIDLSGYGAKVEVYDGVELNDKNQFK	LTSSANSKIRATONONIIFNSVPLDFSVSP	WIRIPKYKNDGIONYIHNEYTIINCMKNNS
Whelan_M81186	211 INDITITIEMPH KINSELLINKI LLINKI	NUMBEL DESCRIGARY BY Y DGV ELNDRNUFR	LTSSANSKIRMTONONIIFNSVPLDFSVSP	WIRIDKYKNING IONY I HNRYTT I NOWKNING
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	961 990	991 1020	1021 1050	1051
Original Seq42	GWKISIRG RIIWTLIDINGKTKSVFFEYN	TREDISKY INDWFFVT TTNNI MNAKIY INC.	KI.ECKTDIKDIDENIANCELIEVI DODIDE	TOPTHWYVEST DIFFET COCKE PERUNTORY
Substitute_Seq42	GWKISIKGNRIIWILIDINGKTKSVFFEYN	IREDISEYINRWFFVTITNNLNNAKIYING	KLESHTD1KD1REV1ANGR11RK1.DGD1DD	TORIUMEVECT PATER COCNIERDVETOCV
Amended_Seq42	G*KISIKGNKIIWILIDINGKIKSVPPEYN	IREDISEYINRWFFVTITNNLNNAKIYING	KIRSHTDIKDIPEVIANCE LIPKI DODINE	TODIUMVVDCI DUTTOI COCUIEDDVVIACV
Whelan_M81186	GWKISIRGNRIIWTLIDINGKTKSVFFEYN	IREDISEYINRWFFVTITNNLNNAKIYING	KLESHTDIKDIREVIANGRIIRKINGDID	TOPTHMEVECT PRITEL COCKIT PEDVETORY
	LEGICALE PROPERTY LINEAR ALLEGA			*******************************
	1081 1110	1111 1140	1141 1170	1171
Original Seq42			YIGEKFIIRRKSNSQSINDDIVRKEDYIYL	1171 1200
Substitute_Seq42	Seylkdfwgnplmynkeyymfnagnknsy	IKLKKDSPVGEILTRSKYNONSKYINYRDL	YIGEKFI IRRKSNSQS INDDIVRKEDYIYL	DPFNINOEWRVYTYKYPKKEREET.PT.ADIC
Amended_Seq42	SKYLKDFWGNPLMYNKEYYMFNAGNKNSYE	I KLKKDSPVGBILTRSKYNONSKY I NYRDI.	YIGEKELLERKSNSOS INDDIVEKENVIVI	DEPAR MORMOUVEVEVEVEVERED IN A DIC
Whelan_M81186	SEYLKDFWGNPLMYNKEYYMFNAGNKNSY	IKLKKOSPVGEILTRSKYNONSKY INYRDL	YIGRKPITERKSNSOSINDDIVEREDVIVI.	DEPAIL MORNOUVTVEVERERERI, PLADIC
		***************************************	900000000000000000000000000000000000000	***************************************
	1201 1230	1231 1260	1261	1202
Original_Seq42	DSDEFYNTIQIKEYDEOPTYSCOLLPKKDE	ESTDEIGLIGIHRPYESGIVPREUKDUPCI	SHWY FEUR REVINE RECEIVED TO THE COMPANY DEPORTS	TP
Substitute_Seq42	DODELANTIOTKEADEONLASCOFTAKKDE	ESTDEIGLIGIHRPYESGIVPEEMKDMPCI	SKWYLKEVKRKPYNLKLGCNWOP I PKDECW	TE
Amended_Seq42				
Whelan_M81186	DSDEFINITUIKEYDEOPTYSCOLLFKKDR	RSTDRIGLIGIUS PYRSGIVE FRANCOURCE	CMMVI.MPUKDKOVNI KI CONMODIOVNOCH	TO TO
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